



PCT09

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/980,862

DATE: 06/05/2002
TIME: 17:29:50

Input Set : A:\29029101.app
Output Set: N:\CRF3\06052002\I980862.raw

P.6

3 <110> APPLICANT: SCHLEHUBER, STEFFEN
5 <120> TITLE OF INVENTION: MUTEINS OF THE BILIN-BINDING PROTEIN
7 <130> FILE REFERENCE: 029029/0101
9 <140> CURRENT APPLICATION NUMBER: 09/980,862
10 <141> CURRENT FILING DATE: 2002-05-06
12 <150> PRIOR APPLICATION NUMBER: DE 199 26 068.0
13 <151> PRIOR FILING DATE: 1999-06-08
15 <160> NUMBER OF SEQ ID NOS: 27
17 <170> SOFTWARE: PatentIn Ver. 2.1
19 <210> SEQ ID NO: 1
20 <211> LENGTH: 1219
21 <212> TYPE: DNA
22 <213> ORGANISM: Artificial Sequence
24 <220> FEATURE:
25 <223> OTHER INFORMATION: Description of Artificial Sequence: pBBP20
26 nucleic acid sequence
28 <220> FEATURE:
29 <221> NAME/KEY: sig_peptide
30 <222> LOCATION: (22)..(84)
32 <220> FEATURE:
33 <221> NAME/KEY: mat_peptide
34 <222> LOCATION: (85)..(1209)
35 <223> OTHER INFORMATION: fusion protein of bilin-binding protein, Strep-tag II
36 and fragment of phage coat protein pIII
38 <220> FEATURE:
39 <221> NAME/KEY: CDS
40 <222> LOCATION: (85)..(606)
41 <223> OTHER INFORMATION: mature bilin-binding protein
43 <220> FEATURE:
44 <221> NAME/KEY: CDS
45 <222> LOCATION: (607)..(636)
46 <223> OTHER INFORMATION: Strep-tag II-affinity tag
48 <220> FEATURE:
49 <221> NAME/KEY: misc_feature
50 <222> LOCATION: (637)..(639)
51 <223> OTHER INFORMATION: amber stop codon
53 <220> FEATURE:
54 <221> NAME/KEY: CDS
55 <222> LOCATION: (640)..(1209)
56 <223> OTHER INFORMATION: amino acids 217-406 of coat protein pIII
58 <400> SEQUENCE: 1
59 tctagttaac gagggcaaaa a atg aaa aag aca gct atc gcg att gca gtg 51
60 Met Lys Lys Thr Ala Ile Ala Ile Ala Val

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61	-20	-15	
63	gca ctg gct ggt ttc gct acc gta gcg cag gcc gac gtg tac cac gac	99	
64	Ala Leu Ala Gly Phe Ala Thr Val Ala Gln Ala Asp Val Tyr His Asp		
65	-10 -5 -1 1 5		
67	ggt gcc tgt ccc gaa gtc aag cca gtc gac aac ttc gac tgg tcc cag	147	
68	Gly Ala Cys Pro Glu Val Lys Pro Val Asp Asn Phe Asp Trp Ser Gln		
69	10 15 20		
71	tac cat ggt aaa tgg tgg gaa gtc gcc aaa tac ccc aac tca gtt gag	195	
72	Tyr His Gly Lys Trp Trp Glu Val Ala Lys Tyr Pro Asn Ser Val Glu		
73	25 30 35		
75	aag tac gga aag tgc gga tgg gct gag tac act cct gaa ggc aag agt	243	
76	Lys Tyr Gly Lys Cys Gly Trp Ala Glu Tyr Thr Pro Glu Gly Lys Ser		
77	40 45 50		
79	gtc aaa gtt tcg aac tac cac gta atc cac ggc aag gaa tac ttt att	291	
80	Val Lys Val Ser Asn Tyr His Val Ile His Gly Lys Glu Tyr Phe Ile		
81	55 60 65		
83	gaa gga act gcc tac cca gtt ggt gac tcc aag att gga aag atc tac	339	
84	Glu Gly Thr Ala Tyr Pro Val Gly Asp Ser Lys Ile Gly Lys Ile Tyr		
85	70 75 80 85		
87	cac agc ctg act tac gga ggt gtc acc aag gag aac gta ttc aac gta	387	
88	His Ser Leu Thr Tyr Gly Gly Val Thr Lys Glu Asn Val Phe Asn Val		
89	90 95 100		
91	ctc tcc act gac aac aag aac tac atc atc gga tac tac tgc aaa tac	435	
92	Leu Ser Thr Asp Asn Lys Asn Tyr Ile Ile Gly Tyr Tyr Cys Lys Tyr		
93	105 110 115		
95	gac gag gac aag aag gga cac caa gac ttc gtc tgg gtg ctc tcc aga	483	
96	Asp Glu Asp Lys Gly His Gln Asp Phe Val Trp Val Leu Ser Arg		
97	120 125 130		
99	agc atg gtc ctt act ggt gaa gcc aag acc gct gtc gag aac tac ctt	531	
100	Ser Met Val Leu Thr Gly Glu Ala Lys Thr Ala Val Glu Asn Tyr Leu		
101	135 140 145		
103	atc ggc tcc cca gta gtc gac tcc cag aaa ctg gta tac agt gac ttc	579	
104	Ile Gly Ser Pro Val Val Asp Ser Gln Lys Leu Val Tyr Ser Asp Phe		
105	150 155 160 165		
107	tct gaa gcc gcc tgc aag gtc aac aat agc aac tgg tct cac ccg cag	627	
108	Ser Glu Ala Ala Cys Lys Val Asn Asn Ser Asn Trp Ser His Pro Gln		
109	170 175 180		
111	tcc gaa aaa tag gct ggc ggc tct ggt ggt tct ggc ggc ggc	675	
112	Phe Glu Lys Gln Ala Gly Gly Ser Gly Gly Ser Gly Gly Gly		
113	185 190 195		
115	tct gag ggt ggt ggc tct gag ggt ggc ggt tct gag ggt ggc ggc tct	723	
116	Ser Glu Gly Gly Ser Glu Gly Gly Ser Glu Gly Gly Ser Gly Ser		
117	200 205 210		
119	gag gga ggc ggt tcc ggt ggt ggc tct ggt tcc ggt gat ttt gat tat	771	
120	Glu Gly Gly Ser Gly Gly Ser Gly Ser Gly Asp Phe Asp Tyr		
121	215 220 225		
123	gaa aag atg gca aac gct aat aag ggg gct atg acc gaa aat gcc gat	819	
124	Glu Lys Met Ala Asn Ala Asn Lys Gly Ala Met Thr Glu Asn Ala Asp		
125	230 235 240 245		

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127 gaa aac gcg cta cag tct gac gct aaa ggc aaa ctt gat tct gtc gct	867
128 Glu Asn Ala Leu Gln Ser Asp Ala Lys Gly Lys Leu Asp Ser Val Ala	
129 250 255 260	
131 act gat tac ggt gct gct atc gat ggt ttc att ggt gac gtt tcc ggc	915
132 Thr Asp Tyr Gly Ala Ala Ile Asp Gly Phe Ile Gly Asp Val Ser Gly	
133 265 270 275	
135 ctt gct aat ggt aat ggt gct act ggt gat ttt gct ggc tct aat tcc	963
136 Leu Ala Asn Gly Asn Gly Ala Thr Gly Asp Phe Ala Gly Ser Asn Ser	
137 280 285 290	
139 caa atg gct caa gtc ggt gac ggt gat aat tca cct tta atg aat aat	1011
140 Gln Met Ala Gln Val Gly Asp Gly Asp Asn Ser Pro Leu Met Asn Asn	
141 295 300 305	
143 ttc cgt caa tat tta cct tcc ctc cct caa tcg gtt gaa tgt cgc cct	1059
144 Phe Arg Gln Tyr Leu Pro Ser Leu Pro Gln Ser Val Glu Cys Arg Pro	
145 310 315 320 325	
147 ttt gtc ttt ggc gct ggt aaa cca tat gaa ttt tct att gat tgt gac	1107
148 Phe Val Phe Gly Ala Gly Lys Pro Tyr Glu Phe Ser Ile Asp Cys Asp	
149 330 335 340	
151 aaa ata aac tta ttc cgt ggt gtc ttt gcg ttt ctt tta tat gtt gcc	1155
152 Lys Ile Asn Leu Phe Arg Gly Val Phe Ala Phe Leu Leu Tyr Val Ala	
153 345 350 355	
155 acc ttt atg tat gta ttt tct acg ttt gct aac ata ctg cgt aat aag	1203
156 Thr Phe Met Tyr Val Phe Ser Thr Phe Ala Asn Ile Leu Arg Asn Lys	
157 360 365 370	
159 gag tct taataagott	1219
160 Glu Ser	
161 375	
164 <210> SEQ ID NO: 2	
165 <211> LENGTH: 64	
166 <212> TYPE: DNA	
167 <213> ORGANISM: Artificial Sequence	
169 <220> FEATURE:	
170 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer	
172 <220> FEATURE:	
173 <221> NAME/KEY: modified_base	
174 <222> LOCATION: (35)..(36) /	
175 <223> OTHER INFORMATION: a, t, c, g, other or unknown	
177 <220> FEATURE:	
178 <221> NAME/KEY: modified_base /	
179 <222> LOCATION: (38) /	
180 <223> OTHER INFORMATION: a, t, c, g, other or unknown	
182 <220> FEATURE:	
183 <221> NAME/KEY: modified_base	
184 <222> LOCATION: (41)..(42) /	
185 <223> OTHER INFORMATION: a, t, c, g, other or unknown	
187 <220> FEATURE:	
188 <221> NAME/KEY: modified_base /	
189 <222> LOCATION: (44)..(45) /	
190 <223> OTHER INFORMATION: a, t, c, g, other or unknown	

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192 <400> SEQUENCE: 2
W4-> 193 ccatggtaaa tgggtggaaag tcgccaaata ccccnknms nnsnnkaagt acggaaagtg 60
194 cgga 64
197 <210> SEQ ID NO: 3
198 <211> LENGTH: 71
199 <212> TYPE: DNA
200 <213> ORGANISM: Artificial Sequence
202 <220> FEATURE:
203 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer
205 <220> FEATURE:
206 <221> NAME/KEY: modified_base
207 <222> LOCATION: (19)..(20) /
208 <223> OTHER INFORMATION: a, t, c, g, other or unknown
210 <220> FEATURE:
211 <221> NAME/KEY: modified_base
212 <222> LOCATION: (46)..(47) /
213 <223> OTHER INFORMATION: a, t, c, g, other or unknown
215 <220> FEATURE:
216 <221> NAME/KEY: modified_base
217 <222> LOCATION: (52)..(53) /
218 <223> OTHER INFORMATION: a, t, c, g, other or unknown
220 <400> SEQUENCE: 3
W4-> 221 gggtaggcgg taccttcsnn aaagtattcc ttgcgtgga ttacmnngta snncgaaact 60
222 ttgacactct t 71
225 <210> SEQ ID NO: 4
226 <211> LENGTH: 74
227 <212> TYPE: DNA
228 <213> ORGANISM: Artificial Sequence
230 <220> FEATURE:
231 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer
233 <220> FEATURE:
234 <221> NAME/KEY: modified_base
235 <222> LOCATION: (27)..(28) /
236 <223> OTHER INFORMATION: a, t, c, g, other or unknown
238 <220> FEATURE:
239 <221> NAME/KEY: modified_base
240 <222> LOCATION: (33)..(34) /
241 <223> OTHER INFORMATION: a, t, c, g, other or unknown
243 <220> FEATURE:
244 <221> NAME/KEY: modified_base
245 <222> LOCATION: (42)..(43) /
246 <223> OTHER INFORMATION: a, t, c, g, other or unknown
248 <220> FEATURE:
249 <221> NAME/KEY: modified_base /
250 <222> LOCATION: (54)..(55)
251 <223> OTHER INFORMATION: a, t, c, g, other or unknown
253 <400> SEQUENCE: 4
W4-> 254 ccaagattgg aaagatctac cacagcnnsa ctnnkggagg tnnnsaccvvs gagnnkgtat 60
255 tcaacgtact ctcc 74

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258 <210> SEQ ID NO: 5
259 <211> LENGTH: 78
260 <212> TYPE: DNA
261 <213> ORGANISM: Artificial Sequence
263 <220> FEATURE:
264 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer
266 <220> FEATURE:
267 <221> NAME/KEY: modified_base /
268 <222> LOCATION: (20)..(21)
269 <223> OTHER INFORMATION: a, t, c, g, other or unknown
271 <220> FEATURE:
272 <221> NAME/KEY: modified_base
273 <222> LOCATION: (26)..(27)
274 <223> OTHER INFORMATION: a, t, c, g, other or unknown
276 <220> FEATURE:
277 <221> NAME/KEY: modified_base
278 <222> LOCATION: (53)..(54)
279 <223> OTHER INFORMATION: a, t, c, g, other or unknown
281 <220> FEATURE:
282 <221> NAME/KEY: modified_base
283 <222> LOCATION: (59)..(60)
284 <223> OTHER INFORMATION: a, t, c, g, other or unknown
286 <400> SEQUENCE: 5
W-5 > 287 tctggagagc acccagacmn ngtcsnngtg tcccttcttg tcctcgtcgt asnngcamnn 60
288 gtatccgatg atgttagtt 78
291 <210> SEQ ID NO: 6
292 <211> LENGTH: 36
293 <212> TYPE: DNA
294 <213> ORGANISM: Artificial Sequence
296 <220> FEATURE:
297 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer
299 <400> SEQUENCE: 6
300 cttcgactgg tcccagtacc atggtaaatg gtggga 36
303 <210> SEQ ID NO: 7
304 <211> LENGTH: 37
305 <212> TYPE: DNA
306 <213> ORGANISM: Artificial Sequence
308 <220> FEATURE:
309 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer
311 <400> SEQUENCE: 7
312 caccagtaag gaccatgctt ctggagagca cccagac 37
315 <210> SEQ ID NO: 8
316 <211> LENGTH: 46
317 <212> TYPE: DNA
318 <213> ORGANISM: Artificial Sequence
320 <220> FEATURE:
321 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
322 oligodeoxynucleotide
324 <400> SEQUENCE: 8

RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/09/980,862

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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:2; N Pos. 35,36,38,41,42,44,45
Seq#:3; N Pos. 19,20,46,47,52,53
Seq#:4; N Pos. 27,28,33,34,42,43,54,55
Seq#:5; N Pos. 20,21,26,27,53,54,59,60
Seq#:13; N Pos. 29,30,38,39,47,48,50,51,53,54,56,57

Invalid Line Length:

The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:16; Line(s) 881